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SEQUENCE LISTING

<110> Japan as represented by Director-General of Agency of Industrial Science and Technology

<120> A thermostable enzyme having aminotransferase activity and a gene coding the enzyme

<130> PH-640-PCT

<160> 2

<210> 1

<211> 389

<212> PRT

<213> Pyrococcus horikoshi

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Lys Leu Phe Asp Ile Ala Ala Gly Met Lys Asp Val Ile Ser Leu Gly

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25

30

Ile Gly Glu Pro Asp Phe Asp Thr Pro Gln His Ile Lys Glu Tyr Ala

35

40

45

Lys Glu Ala Leu Asp Lys Gly Leu Thr His Tyr Gly Pro Asn Ile Gly

50

55

60

Leu Leu Glu Leu Arg Glu Ala Ile Ala Glu Lys Leu Lys Lys Gln Asn
65 70 75 80

Gly Ile Glu Ala Asp Pro Lys Thr Glu Ile Met Val Leu Leu Gly Ala
85 90 95

Asn Gln Ala Phe Leu Met Gly Leu Ser Ala Phe Leu Lys Asp Gly Glu
100 105 110

Glu Val Leu Ile Pro Thr Pro Ala Phe Val Ser Tyr Ala Pro Ala Val
115 120 125

Ile Leu Ala Gly Gly Lys Pro Val Glu Val Pro Thr Tyr Glu Glu Asp
130 135 140

Glu Phe Arg Leu Asn Val Asp Glu Leu Lys Lys Tyr Val Thr Asp Lys
145 150 155 160

Thr Arg Ala Leu Ile Ile Asn Ser Pro Cys Asn Pro Thr Gly Ala Val
165 170 175

Leu Thr Lys Lys Asp Leu Glu Glu Ile Ala Asp Phe Val Val Glu His
180 185 190

Asp Leu Ile Val Ile Ser Asp Glu Val Tyr Glu His Phe Ile Tyr Asp
195 200 205

Asp Ala Arg His Tyr Ser Ile Ala Ser Leu Asp Gly Met Phe Glu Arg

210

215

220

Thr Ile Thr Val Asn Gly Phe Ser Lys Thr Phe Ala Met Thr Gly Trp

225

230

235

240

Arg Leu Gly Phe Val Ala Ala Pro Ser Trp Ile Ile Glu Arg Met Val

245

250

255

Lys Phe Gln Met Tyr Asn Ala Thr Cys Pro Val Thr Phe Ile Gln Tyr

260

265

270

Ala Ala Ala Lys Ala Leu Lys Asp Glu Arg Ser Trp Lys Ala Val Glu

275

280

285

Glu Met Arg Lys Glu Tyr Asp Arg Arg Arg Lys Leu Val Trp Lys Arg

290

295

300

Leu Asn Glu Met Gly Leu Pro Thr Val Lys Pro Lys Gly Ala Phe Tyr

305

310

315

320

Ile Phe Pro Arg Ile Arg Asp Thr Gly Leu Thr Ser Lys Lys Phe Ser

325

330

335

Glu Leu Met Leu Lys Glu Ala Arg Val Ala Val Val Pro Gly Ser Ala

340

345

350

Phe Gly Lys Ala Gly Glu Gly Tyr Val Arg Ile Ser Tyr Ala Thr Ala

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Tyr Glu Lys Leu Glu Glu Ala Met Asp Arg Met Glu Arg Val Leu Lys

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375

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Glu Arg Lys Leu Val

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<212> DNA

<213> Pyrococcus horikoshi

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10

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Lys Leu Phe Asp Ile Ala Ala Gly Met Lys Asp Val Ile Ser Leu Gly

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ata ggg gaa cct gat ttt gat acg cct caa cat att aag gag tat gcc 144

Ile Gly Glu Pro Asp Phe Asp Thr Pro Gln His Ile Lys Glu Tyr Ala

35

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aag gaa gcc ctg gat aag gga ttg act cat tat ggt cca aat ata ggg 192

Lys Glu Ala Leu Asp Lys Gly Leu Thr His Tyr Gly Pro Asn Ile Gly

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ctt tta gag ctt agg gaa gcc ata gct gaa aag tta aag aag cag aat 240

Leu Leu Glu Leu Arg Glu Ala Ile Ala Glu Lys Leu Lys Lys Gln Asn

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75

80

ggc ata gag gct gat cca aag aca gag ata atg gtc tta tta ggt gcg 288

Gly Ile Glu Ala Asp Pro Lys Thr Glu Ile Met Val Leu Leu Gly Ala

85

90

95

aac caa gct ttc tta atg ggc ctc tcg gct ttt ctt aag gat ggt gaa 336

Asn Gln Ala Phe Leu Met Gly Leu Ser Ala Phe Leu Lys Asp Gly Glu

100

105

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Glu Val Leu Ile Pro Thr Pro Ala Phe Val Ser Tyr Ala Pro Ala Val

115

120

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Ile Leu Ala Gly Gly Lys Pro Val Glu Val Pro Thr Tyr Glu Glu Asp

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140

gaa ttc agg cta aac gtt gat gag ctt aaa aag tat gtt acc gac aag 480

Glu Phe Arg Leu Asn Val Asp Glu Leu Lys Lys Tyr Val Thr Asp Lys

145

150

155

160

act aga gct tta ata ata aac tca ccg tgt aat cca acg gga gca gtc 528

Thr Arg Ala Leu Ile Ile Asn Ser Pro Cys Asn Pro Thr Gly Ala Val

165

170

175

tta act aag aaa gat cta gaa gag ata gcg gat ttt gtc gtt gaa cat 576

Leu Thr Lys Lys Asp Leu Glu Glu Ile Ala Asp Phe Val Val Glu His

gat cta att gta ata agc gat gaa gtt tat gag cac ttc att tac gat 624

Asp Leu Ile Val Ile Ser Asp Glu Val Tyr Glu His Phe Ile Tyr Asp

195

200

205

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Asp Ala Arg His Tyr Ser Ile Ala Ser Leu Asp Gly Met Phe Glu Arg

210

215

220

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Thr Ile Thr Val Asn Gly Phe Ser Lys Thr Phe Ala Met Thr Gly Trp

225

230

235

240

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Arg Leu Gly Phe Val Ala Ala Pro Ser Trp Ile Ile Glu Arg Met Val

245

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Lys Phe Gln Met Tyr Asn Ala Thr Cys Pro Val Thr Phe Ile Gln Tyr

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Ala Ala Ala Lys Ala Leu Lys Asp Glu Arg Ser Trp Lys Ala Val Glu

275

280

285

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Glu Met Arg Lys Glu Tyr Asp Arg Arg Arg Lys Leu Val Trp Lys Arg

290

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 Leu Asn Glu Met Gly Leu Pro Thr Val Lys Pro Lys Gly Ala Phe Tyr
 305 310 315 320

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 Ile Phe Pro Arg Ile Arg Asp Thr Gly Leu Thr Ser Lys Lys Phe Ser
 325 330 335

gag ctc atg ctt aaa gaa gct agg gtt gca gta gtt cca ggt agt gcc 1056
 Glu Leu Met Leu Lys Glu Ala Arg Val Ala Val Val Pro Gly Ser Ala
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 Phe Gly Lys Ala Gly Glu Gly Tyr Val Arg Ile Ser Tyr Ala Thr Ala
 355 360 365

tat gag aag ctt gaa gag gcc atg gat aga atg gaa agg gtg tta aag 1152
 Tyr Glu Lys Leu Glu Glu Ala Met Asp Arg Met Glu Arg Val Leu Lys
 370 375 380

gag agg aag cta gtt taa 1170
 Glu Arg Lys Leu Val
 385 389